

Shuter

Errors Corrected by the STIC Systems Branch

Serial Number:

09/724,693A

CRF Processing Date: 2/14/2001

Edited by:

Verified by:

(STIC staff)

ENTERED

☐

Changed a file from non-ASCII to ASCII

☐

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐

Edited a format error in the Current Application Data section, specifically:

☐

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other

☐

Added the mandatory heading and subheadings for "Current Application Data".

☐

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

☐

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☐

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐

Inserted colons after headings/subheadings. Headings edited included:

☐

Deleted extra, invalid, headings used by an applicant, specifically:

☐

Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as

☐

Inserted mandatory headings, specifically:

☐

Corrected an obvious error in the response, specifically:

☐

Edited identifiers where upper case is used but lower case is required, or vice versa.

☐

Corrected an error in the Number of Sequences field, specifically:

☐

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐

Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected:

☒

Other:

Seq 8 - corrected amino acid nos.

RECEIVED

FEB 20 2001

TECH CENTER 1600/2900

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING DATE: 02/14/2001
 PATENT APPLICATION: US/09/724,693A TIME: 10:38:17

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\02142001\I724693A.raw

SEQUENCE LISTING

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C--> 4 (1) GENERAL INFORMATION:
      6 (i) APPLICANT: Hadlaczky, Gyula
      7 Szalay, Aladar
C--> 9 (ii) TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
      10 AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
      12 (iii) NUMBER OF SEQUENCES: 34
      14 (iv) CORRESPONDENCE ADDRESS:
      15 (A) ADDRESSEE: Heller Ehrman White & McAuliffe
      16 (B) STREET: 4250 Executive Square, 7th Floor
      17 (C) CITY: La Jolla
      18 (D) STATE: CA
      19 (E) COUNTRY: USA
      20 (F) ZIP: 92037
      22 (v) COMPUTER READABLE FORM:
      23 (A) MEDIUM TYPE: Diskette
      24 (B) COMPUTER: IBM Compatible
      25 (C) OPERATING SYSTEM: DOS
      26 (D) SOFTWARE: FastSEQ Version 1.5
      28 (vi) CURRENT APPLICATION DATA:
C--> 29 (A) APPLICATION NUMBER: US/09/724,693A
C--> 30 (B) FILING DATE: 28-Nov-2000
      50 (C) CLASSIFICATION:
C--> 47 (vii) PRIOR APPLICATION DATA:
      33 (A) APPLICATION NUMBER: 08/835,682
      34 (B) FILING DATE: 10-APR-1997
      38 (A) APPLICATION NUMBER: 08/695,191
      39 (B) FILING DATE: 07-AUG-1996
      43 (A) APPLICATION NUMBER: 08/682,080
      44 (B) FILING DATE: 15-JUL-1996
      48 (A) APPLICATION NUMBER: 08/629,822
      49 (B) FILING DATE: 10-APR-1996
      52 (viii) ATTORNEY/AGENT INFORMATION:
      53 (A) NAME: Seidman, Stephanie L
      54 (B) REGISTRATION NUMBER: 33,779
      55 (C) REFERENCE/DOCKET NUMBER: 24601-402G
      58 (ix) TELECOMMUNICATION INFORMATION:
      59 (A) TELEPHONE: 858-450-8403
      60 (B) TELEFAX: 858-587-5360
      61 (C) TELEX:
      63 (2) INFORMATION FOR SEQ ID NO: 1:
      65 (i) SEQUENCE CHARACTERISTICS:
      66 (A) LENGTH: 1293 base pairs
      67 (B) TYPE: nucleic acid
      68 (C) STRANDEDNESS: single
      69 (D) TOPOLOGY: linear
      71 (ii) MOLECULE TYPE: Genomic DNA
  
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72      (iii) HYPOTHETICAL: NO
C--> 73      (iv) ANTI-SENSE: NO
W--> 74      (v) FRAGMENT TYPE:
75      (vi) ORIGINAL SOURCE:
76      (ix) FEATURE:
78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
80 GAATTCATCA TTTTTCANGT CCTCAAGTGG ATGTTTCTCA TTTNCCATGA TTTTAAGTTT      60
81 TCTCGCCATA TTCCTGGTCC TACAGTGTGC ATTTCTCCAT TTTNCACGTT TTNCAGTGAT      120
82 TTCGTCATTT TCAAGTCCTC AAGTGGATGT TTCTCATTTN CCATGAATTT CAGTTTTCTN      180
83 GCCATATTCC ACGTCCTACA GNGGACATTT CTAAATTTNC CACCTTTTTC AGTTTTCTC      240
84 GCCATATTTT ACGTCCTAAA ATGTGTATTT CTCGTTTNC GTGATTTTCA GTTTTCTCGC      300
85 CAGATTCCAG GTCCTATAAT GTGCATTTCT CATTTNNCAC GTTTTTCAGT GATTTCGTCA      360
86 TTTTTTCAAG TCGGCAAGTG GATGTTTCTC ATTTNCCATG ATTTNCAGTT TTCTTGNAAT      420
87 ATTCCATGTC CTACAATGAT CATTTTAAAT TTTCCACCTT TTCATTTTTC CACGCCATAT      480
88 TTCATGTCCT AAAGTGTATA TTTCTCCTTT TCCGCGATTT TCAGTTTTCT CGCCATATTC      540
89 CAGGTCCTAC AGTGTGCATT CCTCATTTT CACCTTTTTC ACTGATTTTC TCATTTTTC      600
90 AGTCGTCAAC TGGATCTTTC TAATTTTCCA TGATTTTCAG TTATCTTGTC ATATTCCATG      660
91 TCCTACAGTG GACATTTCTA AATTTTCCAA CTTTTTCAAT TTTTCTCGAC ATATTTGACG      720
92 TGCTAAAGTG TGTATTTCTT ATTTTCCGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGTC      780
93 CTAATAGTGT GCATTTCTCA TTTTTCACGT TTTTCAGTGA TTTCGTCATT TTTTCCAGTT      840
94 GTC AAGGGGA TGTTCCTCAT TTTCCATGAG TGTCAGTTTT CTGCTATAT TCCATGTCCT      900
95 ACAGTGACAT TTCTAAATAT TATACCTTTT TCAGTTTTTC TCACCATATT TCACGTCCTA      960
96 AAGTATATAT TTCTCATTTT CCCTGATTTT CAGTTTCCTT GCCATATTCC AGGTCCTACA      1020
97 GTGTGCATTT CTCATTTTTC ACGTTTTTCA GTAATTTCTT CATTTTTTAA GCCCTCAAAT      1080
98 GGATGTTTCT CATTTTCCAT GATTTTCAGT TTTCTTGCCA TATACCATGT CCTACAGTGG      1140
99 ACATTTCTAA ATTATCCACC TTTTTCAGTT TTTTCATCGG ACATTTTCAG TCCTAAAGTG      1200
100 TGTATTTCTA ATTTTCAGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGAC CTACAGTGTG      1260
101 CATTTCTCAT TTTTCACGTT TTTTCAGTGAA TTC      1293
103 (2) INFORMATION FOR SEQ ID NO: 2:
105      (i) SEQUENCE CHARACTERISTICS:
106          (A) LENGTH: 1044 base pairs
107          (B) TYPE: nucleic acid
108          (C) STRANDEDNESS: single
109          (D) TOPOLOGY: linear
111      (ii) MOLECULE TYPE: Genomic DNA
112      (iii) HYPOTHETICAL: NO
C--> 113      (iv) ANTI-SENSE: NO
W--> 114      (v) FRAGMENT TYPE:
115      (vi) ORIGINAL SOURCE:
116      (ix) FEATURE:
118      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
120 AGGCCTATGG TGAAAAAGGA AATATCTTCC CCTGAAAAC AGACAGAAGG ATTCTCAGAA      60
121 TCTTATTTGT GATGTGCGCC CCTCAACTAA CAGTGTTGAA GCTTTCTTTT GATAGAGCAG      120
122 TTTTGAAACA CTCTTTTGT AAAATCTGCA AGAGGATATT TGGATAGCTT TGAGGATTTT      180
123 CGTTGGAAAC GGGATTGTCT TCATATAAAC CCTAGACAGA AGCATTCTCA GAAGCTTCAT      240
124 TGGGATGTTT CAGTTGAAGT CACAGTGTTG AACAGTCCCC TTTTCATAGAG CAGGTTTGAA      300
125 AACTCTTTT TTGTAGTATC TGGAAGTGGA CATTTGGAGC GATCTCAGGA CTGCGGTGAA      360
126 AAAGGAAATA TCTTCCAATA AAAGCTAGAT AGAGGCAATG TCAGAAACCT TTTTCATGAT      420
127 GTATCTACTC AGCTAACAGA GTTGAACCTT CCTTTGAGAG AGCAGTTTTG AAACACTCTT      480

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128 TTTGTGGAAT CTGCAAGTGG ATATTTGTCT AGCTTTGAGG ATTTTCGTTGG GAAACGGGAT 540
129 TACATATAAA AAGCAGACAG CAGCATTCCC AGAAACTTCT TTGTGATGTT TGCATTCAAG 600
130 TCACAGAGTT GAACATTCCC TTTCATAGAG CAGGTTTGAA ACACACTTTT TGATGTATCT 660
131 GGATGTGGAC ATTTGCAGCG CTTTCAGGCC TAAGGTGAAA AGGAAATATC TTCCCCTGAA 720
132 AACTAGACAG AAGCATTCTC AGAAACTTAT TTGTGATGTG CGCCCTCAAC TAACAGTGTT 780
133 GAAGCTTTCT TTTGATAGAG GCAGTTTTGA AACACTCTTT TGTGGAATCT GCAAGTGGAT 840
134 ATTTGTCTAG CTTTGAGGAT TTCTTTGGAA ACGGGATTAC ATATAAAAAG CAGACAGCAG 900
135 CATTCCCAGA ATCTTGTTTG TGATGTTTGC ATTCAAGTCA CAGAGTTGAA CATTCCCTTT 960
136 CAGAGAGCAG GTTTGAACAC TCTTTTATA GTATCTGGAT GTGGACATTT GGAGCGCTTT 1020
137 CAGGGGGGAT CCTCTAGAAT TCCT 1044
141 (2) INFORMATION FOR SEQ ID NO: 3:
143 (i) SEQUENCE CHARACTERISTICS:
144 (A) LENGTH: 2492 base pairs
145 (B) TYPE: nucleic acid
146 (C) STRANDEDNESS: single
147 (D) TOPOLOGY: linear
149 (ii) MOLECULE TYPE: Genomic DNA
150 (iii) HYPOTHETICAL: NO
C--> 151 (iv) ANTI-SENSE: NO
W--> 152 (v) FRAGMENT TYPE:
153 (vi) ORIGINAL SOURCE:
154 (ix) FEATURE:
156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
158 CTGCAGCTGG GGGTCTCCAA TCAGGCAGGG GCCCCTTACT ACTCAGATGG GGTGGCCGAG 60
159 TAGGGGAAGG GGGTGCAGGC TGCATGAGTG GACACAGCTG TAGGACTACC TGGGGGCTGT 120
160 GGATCTATGG GGGTGGGGAG AAGCCCAGTG ACAGTGCCTA GAAGAGACAA GGTGGCCTGA 180
161 GAGGGTCTGA GGAACATAGA GCTGGCCATG TTGGGGCCAG GTCTCAAGCA GGAAGTGAGG 240
162 AATGGGACAG GCTTGAGGAT ACTCTACTCA GTAGCCAGGA TAGCAAGGAG GGCTTGGGGT 300
163 TGCTATCCTG GGGTTCAACC CCCAGGTTG AAGGCCCTGG GGGAGATGGT CCCAGGACAT 360
164 ATTACAATGG ACACAGGAGG TTGGGACACC TGGAGTCACC AAACAAAACC ATGCCAAGAG 420
165 AGACCATGAG TAGGGGTGTC CAGTCCAGCC CTCTGACTGA GCTGCATTGT TCAAATCCAA 480
166 AGGGCCCCTG CTGCCACCTA GTGGCTGATG GCATCCACAT GACCCTGGGC CACACGCGTT 540
167 TAGGGTCTCT GTGAAGACCA AGATCCTTGT TACATTGAAC GACTCCTAAA TGAGCAGAGA 600
168 TTTCCACCTA TTCGAAACAA TCACATAAAA TCCATCCTGG AAAAAGCCTG GGGGATGGCA 660
169 CTAAGGCTAG GGATAGGGTG GGATGAAGAT TATAGTTACA GTAAGGGGTT TAGGGTTAGG 720
170 GATCAACGTT GGTTAGGAGT TAGGGATACA GTAGGGTACC GGTAGGGTTA GGGGTTAGGG 780
171 TTAGGGGTTA GGGTTAGGGT TAGGGTTAGG GTTAGGGTTA GGGGTTAGGG GTTAGGGTTA 840
172 GGGTTAGGTT TTGGGGTGCC GTATTTTGGT CTTATACGCT GTGTTCCACT GGCAATGAAA 900
173 AGAGTTCTTG TTTTTCCTTC AGCAATTTGT CATTTTAAA AGAGTTTAGC AATTCTAACA 960
174 GATATAGACC AGCTGTGCTA TCTCATTGTG GTTTTCAATT GTAACCACAT TGTGGTTTCA 1020
175 ATGTGTTTAC TTGCCATCTG TAGATCTTCT TTGCGTGAGG TGTCTGTTCA GATGTGTGTG 1080
176 CATTTCTTGN NTTTNGGCTG TTTAACTTAT TGTTTAGTTT TAATAATTTT TTATATATTT 1140
177 GAAGACAAAT CTTTCTCAGA TGTGTATTTG CAAATATTTT TTCAATATGA GGCTTGCTTT 1200
178 TGTCTCTAAC AAGGTCTCTT CAGAGATAAC TTAAATATAA GAAATCCACA CTGTCACTTC 1260
179 TTTTGTGTAT ATCTACCTTT TGTGTCATTT GTTAAAATTC ATTACCAAAC CCAAAGGCAG 1320
180 ATAGCTTTTC TTCTATTGTT TCTTCTAGAA ATTTGTATAG TTTTGCATTT TTAGTGTAAG 1380
181 GATGATTTTG AGTGATTATT TGTGTAAGTT GTAAAGTTTT CGTCTATATC CATATCATTT 1440
182 CTTATGGTTT CCAATTAATC GTTCCCTCAC TATTTTGGG AAAGACACAG GATAGTGGGC 1500
183 TTTGTTAGAG TAGATAGGTA GCTAGACATG AACAGGAGGG GGCCTCCTGG AAAAGGGAAA 1560

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184 GTCTGGGAAG GCTCACCTGG AGGACCACCA AAAATTCACA TATTAGTAGC ATCTCTAGTG 1620
185 CTGGAGTGGA TGGGCACTTG TCAATTGTGG GTAGGAGGGA AAAGAGGTCC TATGCAGAAA 1680
186 GAAACTCCCT AGAACTCCTC TGAAGATGCC CCAATCATTC ACTCTGCAAT AAAAAATGTCA 1740
187 GAATATTGCT AGCTACATGC TGATAAGGNN AAAGGGGACA TTCTTAAGTG AAACCTGGCA 1800
188 CCATAAGTAC AGATTAGGGC AGAGAAGGAC ATTCAAAAGA GGCAGGCGCA GTAGGTACAA 1860
189 ACGTGATCGC TGTCAGTGTG CCTGGGATGG CGGGAAGGAG GCTGGTGCCA GAGTGGATTC 1920
190 GTATTGATCA CCACACATAT ACCTCAACCA ACAGTGAGGA GGTCCCACAA GCCTAAGTGG 1980
191 GGCAAGTTGG GGAGCTAAGG CAGTAGCAGG AAAACCAGAC AAAGAAAACA GGTGGAGACT 2040
192 TGAGACAGAG GCAGGAATGT GAAGAAATCC AAAATAAAAT TCCCTGCACA GGACTCTTAG 2100
193 GCTGTTTAAT GCATCGCTCA GTCCCACTCC TCCCTATTTT TCTACAATAA ACTCTTTACA 2160
194 CTGTGTTTCT TTTCAATGAA GTTATCTGCC ATCTTTGTAT TGCCTCTTGG TGAAAATGTT 2220
195 TCTTCCAAGT TAAACAAGAA CTGGGACATC AGCTCTCCCC AGTAATAGCT CCGTTTCAGT 2280
196 TTGAATTTAC AGAACTGATG GGCTTAATAA CTGGCGCTCT GACTTTAGTG GTGCAGGAGG 2340
197 CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCGCAG GTGGCGGCTG 2400
198 CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGGCGTACG 2460
199 ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG 2492
201 (2) INFORMATION FOR SEQ ID NO: 4:
203 (i) SEQUENCE CHARACTERISTICS:
204 (A) LENGTH: 28 base pairs
205 (B) TYPE: nucleic acid
206 (C) STRANDEDNESS: single
207 (D) TOPOLOGY: linear
209 (ii) MOLECULE TYPE: Genomic DNA
210 (iii) HYPOTHETICAL: NO
C--> 211 (iv) ANTI-SENSE: NO
W--> 212 (v) FRAGMENT TYPE:
213 (vi) ORIGINAL SOURCE:
214 (ix) FEATURE:
216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
218 GGGGAATTCA TTGGGATGTT TCAGTTGA 28
220 (2) INFORMATION FOR SEQ ID NO: 5:
222 (i) SEQUENCE CHARACTERISTICS:
223 (A) LENGTH: 29 base pairs
224 (B) TYPE: nucleic acid
225 (C) STRANDEDNESS: single
226 (D) TOPOLOGY: linear
228 (ii) MOLECULE TYPE: Genomic DNA
229 (iii) HYPOTHETICAL: NO
C--> 230 (iv) ANTI-SENSE: NO
W--> 231 (v) FRAGMENT TYPE:
232 (vi) ORIGINAL SOURCE:
233 (ix) FEATURE:
235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
237 CGAAAGTCCC CCCTAGGAGA TCTTAAGGA 29
239 (2) INFORMATION FOR SEQ ID NO: 6:
241 (i) SEQUENCE CHARACTERISTICS:
242 (A) LENGTH: 47 base pairs
243 (B) TYPE: nucleic acid
244 (C) STRANDEDNESS: single

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Input Set : A:\Pto.amc
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245          (D) TOPOLOGY: linear
W--> 247      (ii) MOLECULE TYPE: DNA
248      (iii) HYPOTHETICAL: NO
C--> 249      (iv) ANTI-SENSE: NO
W--> 250      (v) FRAGMENT TYPE:
251      (vi) ORIGINAL SOURCE:
252      (ix) FEATURE:
254      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
256 CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC      47
260 (2) INFORMATION FOR SEQ ID NO: 7:
262      (i) SEQUENCE CHARACTERISTICS:
263          (A) LENGTH: 25 base pairs
264          (B) TYPE: nucleic acid
265          (C) STRANDEDNESS: single
266          (D) TOPOLOGY: linear
268      (ii) MOLECULE TYPE: Genomic DNA
269      (iii) HYPOTHETICAL: NO
C--> 270      (iv) ANTI-SENSE: NO
W--> 271      (v) FRAGMENT TYPE:
272      (vi) ORIGINAL SOURCE:
273      (ix) FEATURE:
275      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
277 CGATTTAAT TAATTAAGCC CGGGC      25
280 (2) INFORMATION FOR SEQ ID NO: 8:
282      (i) SEQUENCE CHARACTERISTICS:
283          (A) LENGTH: 27 base pairs
284          (B) TYPE: nucleic acid
285          (C) STRANDEDNESS: single
286          (D) TOPOLOGY: linear
288      (ii) MOLECULE TYPE: Genomic DNA
289      (iii) HYPOTHETICAL: NO
C--> 290      (iv) ANTI-SENSE: NO
W--> 291      (v) FRAGMENT TYPE:
292      (vi) ORIGINAL SOURCE:
293      (ix) FEATURE:
295      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
297 TAAATTTAAT TAATTCGGGC CCGTCGA      27
299 (2) INFORMATION FOR SEQ ID NO: 9:
301      (i) SEQUENCE CHARACTERISTICS:
302          (A) LENGTH: 69 base pairs
303          (B) TYPE: nucleic acid
304          (C) STRANDEDNESS: single
305          (D) TOPOLOGY: linear
307      (ii) MOLECULE TYPE: Genomic DNA
310      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
312 ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT      48
313 Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
314 1          5          10          15
316 GTC ACA AAC AGT GCA CCT ACT      69

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Input Set : A:\Pto.amc

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L:4 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:9 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:37 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:42 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:47 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:73 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:78 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1
L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1
L:113 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:118 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=2
L:114 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2
L:151 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:156 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=3
L:152 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3
L:211 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:216 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=4
L:212 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=4
L:230 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:235 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=5
L:231 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=5
L:249 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:254 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=6
L:247 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:250 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6
L:270 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:275 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=7
L:271 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=7
L:290 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:295 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=8
L:291 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8
L:308 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:308 M:220 C: Keyword misspelled or invalid format, Poss data loss, Seq 9, (D) OTHER INFORMATION:
L:340 M:220 C: Keyword misspelled or invalid format, [(H) DOCUMENT NUMBER:]
L:434 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:439 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=11
L:435 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=11
L:453 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:458 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=12
L:454 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=12
L:472 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:473 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=13
L:513 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:514 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=14
L:554 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:555 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=15
L:594 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]

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L:595 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=16
L:980 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:981 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=17
L:1714 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1715 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=18
L:1735 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1736 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=19
L:1765 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1766 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=20
L:1790 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1791 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21
L:1814 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1815 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=22
L:1838 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1839 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=23
L:1867 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1868 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=24
L:1897 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1898 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=25
L:1915 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1916 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=26
L:1933 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1934 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=27
L:1951 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1952 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=28
L:1969 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1970 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=29
L:1988 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1989 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=30
L:2006 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2007 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=31
L:2024 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2025 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=32
L:2042 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2043 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=33
L:2060 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2061 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=34